

sequence_listing.ST25
SEQUENCE LISTING

<110> Karolinska Innovations AB
Ingelman-Sundberg, Magnus
Karlgren, Maria
Gomez, Alvin

<120> Drug target in cancer therapy

<130> P05980PC00/HAM/em

<150> SE0203137-5

<151> 2002-10-24

<150> US 60/420,787

<151> 2002-10-24

<160> 10

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Homo sapiens

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Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro Ala Ala Arg Trp Pro
20 25 30

Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg
35 40 45

Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly
50 55 60

Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr
65 70 75 80

Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu
85 90 95

Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly
100 105 110

Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe
115 120 125

Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala
130 135 140

Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly
145 150 155 160

Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser
165 170 175

Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp
180 185 190

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Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu
195 200 205

Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly
210 215 220

Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val
225 230 235 240

Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys
245 250 255

Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly
260 265 270

Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala
275 280 285

Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr
290 295 300

Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly
305 310 315 320

Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro
325 330 335

Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His
340 345 350

Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr
355 360 365

Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro
370 375 380

Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln
385 390 395 400

Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His
405 410 415

Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val
420 425 430

Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala
435 440 445

Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro
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tcaccagcca cgtcctc atg gcc ctg ctg ctc ttg ctg ttc ctg ggc ctc 170
Met Ala Leu Leu Leu Leu Phe Leu Gly Leu
1 5 10
ctg ggg ctc tgg ggg ctg ctc tgc gcc tgc gcc caa gac ccc tcc cca 218
Leu Gly Leu Trp Gly Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro
15 20 25
gct gcc cgg tgg ccc ccg ggg cct cgc ccg ctg ccg ctc gtc ggg aac 266
Ala Ala Arg Trp Pro Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn
30 35 40
ctg cac ttg ctg cgt ctg tcg caa cag gac cgg tcc ctg atg gag ctc 314
Leu His Leu Leu Arg Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu
45 50 55
tca gaa cgc tac ggg ccg gtg ttc acc gtg cac ctg ggg cgc cag aag 362
Ser Glu Arg Tyr Gly Pro Val Phe Thr Val His Leu Gly Arg Gln Lys
60 65 70 75
acg gtg gtg ctg acg ggg ttc gag gcg gtc aaa gag gcg ctg gcg ggc 410
Thr Val Val Leu Thr Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly
80 85 90
ccc ggg cag gag ctg gcc gac cgg cct ccc atc gcc atc ttc cag ctc 458
Sida 6

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gct Ala	gcc Ala 125	cgc Arg	cag Gln	ttc Phe	acg Thr	gtg Val 130	cgt Arg	gcc Ala	ctg Leu	cac His	agc Ser 135	ctg Leu	ggc Gly	gtg Val	ggc Gly		554
cgg Arg 140	gag Glu	ccg Pro	gtg Val	gct Ala	gac Asp 145	aag Lys	att Ile	ctg Leu	cag Gln	gag Glu 150	ctg Leu	aaa Lys	tgc Cys	ctc Leu	tct Ser 155		602
ggg Gly	cag Gln	ctg Leu	gat Asp	ggc Gly 160	tac Tyr	aga Arg	ggc Gly	cgg Arg	ccc Pro 165	ttc Phe	ccg Pro	ctg Leu	gcc Ala	cta Leu 170	ctg Leu		650
ggc Gly	tgg Trp	gct Ala	ccc Pro 175	tcc Ser	aat Asn	atc Ile	acc Thr	ttc Phe 180	gcg Ala	ctc Leu	ctc Leu	ttc Phe	ggc Gly 185	cgc Arg	cga Arg		698
ttt Phe	gac Asp	tac Tyr 190	cgg Arg	gac Asp	ccc Pro	gtg Val	ttt Phe 195	gtg Val	tcc Ser	ctg Leu	ctg Leu	ggt Gly 200	ctc Leu	atc Ile	gat Asp		746
gag Glu	gtc Val 205	atg Met	gtc Val	ctc Leu	ttg Leu	ggg Gly 210	tcc Ser	cct Pro	ggc Gly	ctg Leu	cag Gln 215	ctg Leu	ttc Phe	aac Asn	gtc Val		794
tac Tyr 220	cca Pro	tgg Trp	ctc Leu	ggg Gly	gcc Ala 225	ctg Leu	ctc Leu	cag Gln	ctg Leu	cac His 230	cgg Arg	ccc Pro	gtc Val	ctg Leu	cgc Arg 235		842
aag Lys	atc Ile	gag Glu	gag Glu	gtc Val 240	cgt Arg	gcc Ala	att Ile	ctg Leu	agg Arg 245	acc Thr	ctc Leu	ctg Leu	gag Glu	gcg Ala 250	cgg Arg		890
agg Arg	ccc Pro	cac His	gtg Val 255	tgc Cys	ccg Pro	ggg Gly	gac Asp	ccc Pro 260	gtg Val	tgc Cys	agc Ser	tat Tyr	gtg Val 265	gac Asp	gcc Ala		938
ctg Leu	atc Ile	cag Gln 270	cag Gln	gga Gly	cag Gln	ggg Gly	gat Asp 275	gac Asp	ccc Pro	gag Glu	ggc Gly	ctg Leu 280	ttt Phe	gct Ala	gag Glu		986
gcc Ala 285	aac Asn	gcg Ala	gtg Val	gcc Ala	tgc Cys	acc Thr 290	ctg Leu	gac Asp	atg Met	gtc Val	atg Met 295	gcc Ala	ggg Gly	acg Thr	gag Glu		1034
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ccg Pro	gac Asp	gtg Val	cag Gln	ggc Gly 320	cgg Arg	gtg Val	cag Gln	gag Glu	gag Glu 325	cta Leu	gac Asp	cgc Arg	gtg Val	ctg Leu 330	ggc Gly		1130
cct Pro	ggg Gly	cgg Arg	act Thr 335	ccc Pro	cgg Arg	ctg Leu	gag Glu	gac Asp 340	cag Gln	cag Gln	gct Ala	ctg Leu	ccc Pro 345	tac Tyr	aca Thr		1178
agc Ser	gcc Ala	gtg Val 350	ctc Leu	cac His	gag Glu	gtg Val	cag Gln 355	cgg Arg	ttc Phe	atc Ile	acg Thr	ctc Leu 360	ctg Leu	ccg Pro	cac His		1226
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Ala	Gly	Arg	Arg	Val	Cys	Val	Gly	Glu	Arg	Leu	Ala	Arg	Thr	Glu	Leu	
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Phe	Leu	Leu	Phe	Ala	Gly	Leu	Leu	Gln	Arg	Tyr	Arg	Leu	Leu	Pro	Pro	
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Thr	Met	Arg	Pro	Arg	Ala	Gln	Ala	Leu	Cys	Ala	Val	Pro	Arg	Pro		
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sequence_listing.ST25

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tcaccagcca cgtcctc 137